



SEQUENCE LISTING

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AUG 03 2001
TECH CENTER 1600/2900

<110> De Veylder, Lieven
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Van Camp, Wim
Krols, Luc

<120> Cyclin-dependent kinase inhibitors and uses thereof

<130> 2283/301

<140> US 09/574,735

<141> 2000-05-18

<160> 48

<170> PatentIn version 3.0

<210> 1

<211> 932

<212> DNA

<213> Arabidopsis thaliana

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<222> (86)..(712)

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                               1           5
gat gtg gtt gaa gag aat gga gtt acg acg acg acg gtg aaa cga agg      160
Asp Val Val Glu Glu Asn Gly Val Thr Thr Thr Thr Val Lys Arg Arg
10           15           20           25
aag atg gag gag gaa gtg gat tta gtg gaa tct agg ata att ctg tct      208
Lys Met Glu Glu Glu Val Asp Leu Val Glu Ser Arg Ile Ile Leu Ser
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ccg tgt gta cag gcg acg aat cgc ggt gga att gtg gcg aga aat tca      256
Pro Cys Val Gln Ala Thr Asn Arg Gly Ile Val Ala Arg Asn Ser
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gca gga gcg tcg gag acg agt gtt gtt ata gta cga cgg cga gat tct      304
Ala Gly Ala Ser Glu Thr Ser Val Val Ile Val Arg Arg Arg Asp Ser
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Ser Cys Cys Ser Thr Ser Glu Glu Lys Ser Lys Arg Arg Ile Glu Phe
90           95           100           105
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Val Asp Leu Glu Glu Asn Asn Gly Asp Asp Arg Glu Thr Glu Thr Ser
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140 145 150	
aag agt ctc cat gag acg gtg aag gaa gct gag tta gaa gat ttt ttt	592
Lys Ser Leu His Glu Thr Val Lys Glu Ala Glu Leu Glu Asp Phe Phe	
155 160 165	
cag gtg gcg gag aaa gat ctt cgg aat aag ttg ttg gaa tgt tct atg	640
Gln Val Ala Glu Lys Asp Leu Arg Asn Lys Leu Leu Glu Cys Ser Met	
170 175 180 185	
aag tat aac ttc gat ttc gag aaa gat gag cca ctt ggt gga gga aga	688
Lys Tyr Asn Phe Asp Phe Glu Lys Asp Glu Pro Leu Gly Gly Gly Arg	
190 195 200	
tac gag tgg gtt aaa ttg aat cca tgaagaagac gatgatgata atgatgatca	742
Tyr Glu Trp Val Lys Leu Asn Pro	
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35 40 45
Arg Gly Gly Ile Val Ala Arg Asn Ser Ala Gly Ala Ser Glu Thr Ser
50 55 60
Val Val Ile Val Arg Arg Asp Ser Pro Pro Val Glu Glu Gln Cys
65 70 75 80
Gln Ile Glu Glu Glu Asp Ser Ser Val Ser Cys Cys Ser Thr Ser Glu
85 90 95
Glu Lys Ser Lys Arg Arg Ile Glu Phe Val Asp Leu Glu Glu Asn Asn
100 105 110
Gly Asp Asp Arg Glu Thr Glu Thr Ser Trp Ile Tyr Asp Asp Leu Asn
115 120 125
Lys Ser Glu Glu Ser Met Asn Met Asp Ser Ser Ser Val Ala Val Glu
130 135 140
Asp Val Glu Ser Arg Arg Arg Leu Arg Lys Ser Leu His Glu Thr Val
145 150 155 160
Lys Glu Ala Glu Leu Glu Asp Phe Phe Gln Val Ala Glu Lys Asp Leu
165 170 175
Arg Asn Lys Leu Leu Glu Cys Ser Met Lys Tyr Asn Phe Asp Phe Glu
180 185 190
Lys Asp Glu Pro Leu Gly Gly Gly Arg Tyr Glu Trp Val Lys Leu Asn
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 Ser Lys Ala Thr Ala Pro Ser Pro Gly Val Arg Thr Arg Ala Ala Lys
 15 20 25
 acc cta gcc ttg aag cgg ctt aat tcc tcc gcc gct gat tca gct cta 145
 Thr Leu Ala Leu Lys Arg Leu Asn Ser Ser Ala Ala Asp Ser Ala Leu
 30 35 40 45
 cct aac gac tct tct tgc tat ctt cag ctc cgt agc cgc cgt ctc gag 193
 Pro Asn Asp Ser Ser Cys Tyr Leu Gln Leu Arg Ser Arg Arg Leu Glu
 50 55 60
 aaa ccc tct tcg ctg att gaa ccg aaa cag ccg ccg aga gtt cac aga 241
 Lys Pro Ser Ser Leu Ile Glu Pro Lys Gln Pro Pro Arg Val His Arg
 65 70 75
 tcg gga att aaa gag tct ggt tcc agg tct cgc gtt gac tcg gtt aac 289
 Ser Gly Ile Lys Glu Ser Gly Ser Arg Ser Arg Val Asp Ser Val Asn
 80 85 90
 tcg gtt cct gta gct cag agc tct aat gaa gat gaa tgt ttt gac aat 337
 Ser Val Pro Val Ala Gln Ser Ser Asn Glu Asp Glu Cys Phe Asp Asn
 95 100 105
 ttc gtg agt gtc caa gtt tct tgt ggt gaa aac agt ctc ggt ttt gaa 385
 Phe Val Ser Val Gln Val Ser Cys Gly Glu Asn Ser Leu Gly Phe Glu
 110 115 120 125
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 Ser Arg His Ser Thr Arg Glu Ser Thr Pro Cys Asn Phe Val Glu Asp
 130 135 140
 atg gag atc atg gtt aca cca ggg tct agc acg agg tcg atg tgc aga 481
 Met Glu Ile Met Val Thr Pro Gly Ser Ser Thr Arg Ser Met Cys Arg
 145 150 155
 gca acc aaa gag tac aca agg gaa caa gat aac gtg atc ccg acc act 529
 Ala Thr Lys Glu Tyr Thr Arg Glu Gln Asp Asn Val Ile Pro Thr Thr
 160 165 170
 agt gaa atg gag gag ttc ttt gca tat gca gag cag cag caa cag agg 577
 Ser Glu Met Glu Glu Phe Phe Ala Tyr Ala Glu Gln Gln Gln Arg
 175 180 185
 cta ttc atg gag aag tac aac ttc gac att gtg aat gat atc ccc ctc 625
 Leu Phe Met Glu Lys Tyr Asn Phe Asp Ile Val Asn Asp Ile Pro Leu
 190 195 200 205
 agc gga cgt tac gaa tgg gtg caa gtc aaa cca tgaagttcaa aaggaaacag 678
 Ser Gly Arg Tyr Glu Trp Val Gln Val Lys Pro
 210 215
 ctccaaaaga catggtgtga agttagagaa tgtgatggag ttaacagact aaccaaacat 738
 cagaaatcgt gtaatcttaa gtaataatgt ggtagagaa caagtttgag agtagcttag 798
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      35      40      45
Ser Ala Leu Pro Asn Asp Ser Ser Cys Tyr Leu Gln Leu Arg Ser Arg
      50      55      60
Arg Leu Glu Lys Pro Ser Ser Leu Ile Glu Pro Lys Gln Pro Pro Arg
      65      70      75      80
Val His Arg Ser Gly Ile Lys Glu Ser Gly Ser Arg Ser Arg Val Asp
      85      90      95
Ser Val Asn Ser Val Pro Val Ala Gln Ser Ser Asn Glu Asp Glu Cys
      100     105     110
Phe Asp Asn Phe Val Ser Val Gln Val Ser Cys Gly Glu Asn Ser Leu
      115     120     125
Gly Phe Glu Ser Arg His Ser Thr Arg Glu Ser Thr Pro Cys Asn Phe
      130     135     140
Val Glu Asp Met Glu Ile Met Val Thr Pro Gly Ser Ser Thr Arg Ser
      145     150     155     160
Met Cys Arg Ala Thr Lys Glu Tyr Thr Arg Glu Gln Asp Asn Val Ile
      165     170     175
Pro Thr Thr Ser Glu Met Glu Glu Phe Phe Ala Tyr Ala Glu Gln Gln
      180     185     190
Gln Gln Arg Leu Phe Met Glu Lys Tyr Asn Phe Asp Ile Val Asn Asp
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Ile Pro Leu Ser Gly Arg Tyr Glu Trp Val Gln Val Lys Pro
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                               Met Gly Lys Tyr Met Lys Lys
                               1      5
ctc aaa tcc aaa tca gaa tct cct tca ccc aat tca aca cca aca cca      160
Leu Lys Ser Lys Ser Glu Ser Pro Ser Pro Asn Ser Thr Pro Thr Pro
      10      15      20
tca cca tca cca tca cca aca cca atc acc acc aat tca cca cca cca      208
Ser Pro Ser Pro Ser Pro Thr Pro Ile Thr Thr Asn Ser Pro Pro Pro
      25      30      35
aca aca ccc aat tcc tct gat ggt gtt cga act cgt gct aga acc cta      256
Thr Thr Pro Asn Ser Ser Asp Gly Val Arg Thr Arg Ala Arg Thr Leu
      40      45      50      55
gct ttg gag aat tcc aac aat cag aat cag aat ctt tct gtt tct tct      304
Ala Leu Glu Asn Ser Asn Asn Gln Asn Gln Asn Leu Ser Val Ser Ser
      60      65      70

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Arg Gln His Ser Ala Lys Arg Asn Lys Gly His Asp Gly Asn Pro Lys	
90 95 100	
tcc cca att ggg gat tca att gct gaa gag aaa act gtt cag aag agt	448
Ser Pro Ile Gly Asp Ser Ile Ala Glu Glu Lys Thr Val Gln Lys Ser	
105 110 115	
cct gag cct gaa aat gct gaa ttc aag gag aat gct gag gat act gag	496
Pro Glu Pro Glu Asn Ala Glu Phe Lys Glu Asn Ala Glu Asp Thr Glu	
120 125 130 135	
aga agc gct agg gaa act aca ccc gtc cat ttg ata atg cga gca gac	544
Arg Ser Ala Arg Glu Thr Thr Pro Val His Leu Ile Met Arg Ala Asp	
140 145 150	
gtt ctc agg cct cct agg cca att acc agg cgt act ttt cca act gaa	592
Val Leu Arg Pro Pro Arg Pro Ile Thr Arg Arg Thr Phe Pro Thr Glu	
155 160 165	
gct aat ccc aaa acg gag cag cca act atc cca att tca cgc gaa ttt	640
Ala Asn Pro Lys Thr Glu Gln Pro Thr Ile Pro Ile Ser Arg Glu Phe	
170 175 180	
gag gaa ttc tgt gct aaa cat gaa gcc gag cag caa agg gag ttc atg	688
Glu Glu Phe Cys Ala Lys His Glu Ala Glu Gln Gln Arg Glu Phe Met	
185 190 195	
gag aag tac aac ttt gat cct gtg aca gag cag cca ctc cca ggg cgt	736
Glu Lys Tyr Asn Phe Asp Pro Val Thr Glu Gln Pro Leu Pro Gly Arg	
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Tyr Glu Trp Glu Lys Val Ser Pro	
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tgtatatttcc attttccatc actttctatt tacttgtaaa gaaagtagga ctttcaacat	903
atgtagacta atgatctgta actttacaga ggtgttgatt acacaacaat acaaagtcct	963
ttgtctagca gatcattaaa gaagggtttg aggggaataag ggtctctagt tgtagggttt	1023
aggggtataaa atcaaagtag ggtatgtaag agagggtttta caagaatttc cttttgttct	1083
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50 55 60	
Gln Asn Leu Ser Val Ser Ser Asp Ser Tyr Leu Gln Leu Arg Asn Arg	
65 70 75 80	
Arg Leu Lys Arg Pro Leu Ile Arg Gln His Ser Ala Lys Arg Asn Lys	
85 90 95	
Gly His Asp Gly Asn Pro Lys Ser Pro Ile Gly Asp Ser Ile Ala Glu	
100 105 110	
Glu Lys Thr Val Gln Lys Ser Pro Glu Pro Glu Asn Ala Glu Phe Lys	
115 120 125	

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His	Leu	Ile	Met	Arg	Ala	Asp	Val	Leu	Arg	Pro	Pro	Arg	Pro	Ile	Thr
145					150					155					160
Arg	Arg	Thr	Phe	Pro	Thr	Glu	Ala	Asn	Pro	Lys	Thr	Glu	Gln	Pro	Thr
				165					170					175	
Ile	Pro	Ile	Ser	Arg	Glu	Phe	Glu	Glu	Phe	Cys	Ala	Lys	His	Glu	Ala
			180					185					190		
Glu	Gln	Gln	Arg	Glu	Phe	Met	Glu	Lys	Tyr	Asn	Phe	Asp	Pro	Val	Thr
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<223> Xaa at any of positions 6, 7 or 8 may be any amino acid

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<211> 8
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<211> 9

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 35 40 45
 Thr Arg Ala Lys Ser Leu Ala Leu Gln Gln Gln Gln Gln Arg Cys Leu
 50 55 60
 Leu Gln Lys Pro Ser Ser Pro Ser Ser Leu Pro Pro Thr Ser Ala Ser
 65 70 75 80
 Pro Asn Pro Pro Ser Lys Gln Lys Met Lys Lys Lys Gln Gln Gln Met
 85 90 95
 Asn Asp Cys Gly Ser Tyr Leu Gln Leu Arg Ser Arg Arg Leu Gln Lys
 100 105 110
 Lys Pro Pro Ile Val Val Ile Arg Ser Thr Lys Arg Arg Lys Gln Gln
 115 120 125
 Arg Arg Asn Glu Thr Cys Gly Arg Asn Pro Asn Pro Arg Ser Asn Leu
 130 135 140
 Asp Ser Ile Arg Gly Asp Gly Ser Arg Ser Asp Ser Val Ser Glu Ser
 145 150 155 160
 Val Val Phe Gly Lys Asp Lys Asp Leu Ile Ser Glu Ile Asn Lys Asp
 165 170 175
 Pro Thr Phe Gly Gln Asn Phe Phe Asp Leu Glu Glu Glu His Thr Gln
 180 185 190
 Ser Phe Asn Arg Thr Thr Arg Glu Ser Thr Pro Cys Ser Leu Ile Arg
 195 200 205
 Arg Pro Glu Ile Met Thr Thr Pro Gly Ser Ser Thr Lys Leu Asn Ile
 210 215 220
 Cys Val Ser Glu Ser Asn Gln Arg Glu Asp Ser Leu Ser Arg Ser His
 225 230 235 240
 Arg Arg Arg Pro Thr Thr Pro Glu Met Asp Glu Phe Phe Ser Gly Ala
 245 250 255
 Glu Glu Glu Gln Gln Lys Gln Phe Ile Glu Lys Tyr Val Phe Pro Arg
 260 265 270
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 275 280 285
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12